

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shak, Steven
- (ii) TITLE OF INVENTION: Anti-Infective Therapy
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: 07-Nov-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/669306
 - (B) FILING DATE: 25-Sep-2001
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/873506
 - (B) FILING DATE: 08-Dec-1999
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/643195
 - (B) FILING DATE: 06-May-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/459909
 - (B) FILING DATE: 02-Jun-1995
- (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/191749
(B) FILING DATE: 03-Feb-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/914,226
(B) FILING DATE: 13-Jul-1992

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/448038
(B) FILING DATE: 08-Dec-1989

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/289958
(B) FILING DATE: 23-Dec-1988

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Johnston, Sean A.
(B) REGISTRATION NUMBER: 35,910
(C) REFERENCE/DOCKET NUMBER: P0530P1C10

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-3562
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGCTGGACA CCTACCAGTA TGATGATGGC TGTGAGTCCT GTGGCAATGA 50

C 51

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Asp Thr Tyr Gln Tyr Asp Asp Gly Cys Glu Ser Cys Gly
 1 5 10 15

Asn Asp

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TATGACGTCT ACCTGGACGT GCAGCAGAAG TGGCATCTGA ATGATGTGAT 50
 GCTGATGGGC GACTTCAACG C 71

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Tyr Asp Val Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp
 1 5 10 15

Val Met Leu Met Gly Asp Phe Asn
 20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CC 42

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCGCATGTC CCAGGGCCAC AGGCAGCGTT TCCTGGTAGG AC 42

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGAAGATCG CAGCCTTCAA CATCCAGACA T 31

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTGGATGTTG AAGGVTGCGA TCTTCAATGC A 31

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGAATTAT GTTAAAAATT GCAGCATTTA ATATTCAAAC AT 42

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGAATATTA AATGCTGCAA TTTTAAACAT AATT 34

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Leu Lys Ile Ala Ala Phe
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1039 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCCTGCACAG GCAGTGCCTT GAAGTGCTTC TTCAGAGACC TTTCTTCATA 50

GACTACTTTT TTTTCTTTAA GCAGCAAAAG GAGAAAATTG TCATCAAAGG 100
 ATATTCCAGA TTCTTGACAG CATTCTCGTC ATCTCTGAGG ACATCACCAT 150
 CATCTCAGGA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC 200
 GGCCCTACTG CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC 250
 AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 300
 GTGCAGATCC TGAGCCGCTA TGACATCGCC CTGGTCCAGG AGGTCAGAGA 350
 CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGATG 400
 CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC 450
 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT 500
 GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT 550
 TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 600
 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC 650
 CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG 700
 GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT 750
 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT 800
 CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT 850
 GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGCGCCGTT 900
 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG 950
 TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC 1000
 TGAAGTGAGC AGCCCCTCCC CACACCAGTT GAACTGCAG 1039

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ser	Cys	Thr	Gly	Ser	Ala	Leu	Lys	Cys	Phe	Phe	Arg	Asp	Leu	Ser	1	5	10	15
Ser	Thr	Thr	Phe	Phe	Ser	Leu	Ser	Ser	Lys	Arg	Arg	Lys	Leu	Ser	20	25	30	
Ser	Lys	Asp	Ile	Pro	Asp	Ser	Gln	His	Ser	Arg	His	Leu	Gly	His	35	40	45	
His	His	His	Leu	Arg	Met	Arg	Gly	Met	Lys	Leu	Leu	Gly	Ala	Leu	50	55	60	
Leu	Ala	Leu	Ala	Ala	Leu	Leu	Gln	Gly	Ala	Val	Ser	Leu	Lys	Ile	65	70	75	
Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	Thr	Lys	Met	Ser	Asn	80	85	90	
Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	Ser	Arg	Tyr	Asp	95	100	105	
Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	Thr	Ala	Val	110	115	120	
Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	Thr	Tyr	125	130	135	
His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	Glu	140	145	150	
Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	155	160	165	
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	170	175	180	
Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	185	190	195	
Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	200	205	210	
Asp	Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	215	220	225	

Val	Gln	Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp
				230					235					240
Phe	Asn	Ala	Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser
				245					250					255
Ile	Arg	Leu	Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp
				260					265					270
Ser	Ala	Asp	Thr	Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg
				275					280					285
Ile	Val	Val	Ala	Gly	Met	Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp
				290					295					300
Ser	Ala	Leu	Pro	Phe	Asn	Phe	Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp
				305					310					315
Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp	His	Tyr	Pro	Val	Glu	Val	Met
				320					325					330
Leu	Lys	Ala	Ala	Pro	Pro	His	Thr	Ser	Thr	Ala				
				335					340					

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	Thr	Lys
1				5				10						15
Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	Ser
				20				25						30
Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu
				35				40						45
Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro
				50				55						60

Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	65	70	75
Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	80	85	90
Ala	Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	95	100	105
Asn	Asp	Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	110	115	120
Arg	Phe	Thr	Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	125	130	135
Ala	Pro	Gly	Asp	Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	140	145	150
Tyr	Leu	Asp	Val	Gln	Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	155	160	165
Met	Gly	Asp	Phe	Asn	Ala	Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	170	175	180
Trp	Ser	Ser	Ile	Arg	Leu	Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	185	190	195
Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	200	205	210
Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	Leu	Leu	Arg	Gly	Ala	Val	215	220	225
Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn	Phe	Gln	Ala	Ala	Tyr	Gly	230	235	240
Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp	His	Tyr	Pro	Val	245	250	255
Glu	Val	Met	Leu	Lys											260		

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Arg	Thr	Phe	Gly	Glu	Thr	Lys	1	5	10	15
Met	Ser	Asn	Ala	Thr	Leu	Ala	Ser	Tyr	Ile	Val	Arg	Ile	Val	Arg	20	25	30	
Arg	Tyr	Asp	Ile	Val	Leu	Ile	Glu	Gln	Val	Arg	Asp	Ser	His	Leu	35	40	45	
Val	Ala	Val	Gly	Lys	Leu	Leu	Asp	Tyr	Leu	Asn	Gln	Asp	Asp	Pro	50	55	60	
Asn	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	65	70	75	
Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Leu	Phe	Arg	Pro	Asn	Lys	Val	Ser	80	85	90	
Val	Leu	Asp	Thr	Tyr	Gln	Tyr	Asp	Asp	Gly	Cys	Glu	Ser	Cys	Gly	95	100	105	
Asn	Asp	Ser	Phe	Ser	Arg	Glu	Pro	Ala	Val	Val	Lys	Phe	Ser	Ser	110	115	120	
His	Ser	Thr	Lys	Val	Lys	Glu	Phe	Ala	Ile	Val	Ala	Leu	His	Ser	125	130	135	
Ala	Pro	Ser	Asp	Ala	Val	Ala	Glu	Ile	Asn	Ser	Leu	Tyr	Asp	Val	140	145	150	
Tyr	Leu	Asp	Val	Gln	Gln	Lys	Trp	His	Leu	Asn	Asp	Val	Met	Leu	155	160	165	
Met	Gly	Asp	Phe	Asn	Ala	Asp	Cys	Ser	Tyr	Val	Thr	Ser	Ser	Gln	170	175	180	
Trp	Ser	Ser	Ile	Arg	Leu	Arg	Thr	Ser	Ser	Thr	Phe	Gln	Trp	Leu	185	190	195	
Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr	Ser	Thr	Asn	Cys	Ala				

	200		205		210
Tyr Asp Arg Ile	Val Val Ala Gly Ser	Leu Leu Gln Ser Ser	Val		
	215		220		225
Val Gly Pro Ser	Ala Ala Pro Phe Asp	Phe Gln Ala Ala Tyr	Gly		
	230		235		240
Leu Ser Asn Glu	Met Ala Leu Ala Ile	Ser Asp His Tyr Pro	Val		
	245		250		255
Glu Val Thr Leu Thr					
	260				

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 664 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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TTCGAGCTCG CCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150
CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200
GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250
CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300
CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
GGCTTTTTTG GAGGCCTAGG CTTTGTGAAA AAGCTTATCG GGCCGGGAAC 400
GGTGCAATTGG AACGCGGATT CCCCGTGCCA AGAGTGACGT AAGTACCGCC 450
TATAGAGTCT ATAGGCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500
TTAATACATA ACCTTATGTA TCATACACAT ACGATTTAGG TGACACTATA 550

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GAATAACATC CACTTTGCCT TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC 600
 AACTGCACCT CGGTTCTAAG CTTGGGCTGC AGGTCGCCGT GAATTTAAGG 650
 GACGCTGTGA AGCA 664

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 664 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
 GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
 TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150
 CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200
 GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250
 CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300
 CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
 GGCTTTTTTTG GAGGCCTAGG CTTTTGCAAA AAGCTTATCC GGCCGGGAAC 400
 GGTGCATTGG AACGCGGATT CCCCGTGCCA AGAGTCAGGT AAGTACCGCC 450
 TATAGAGTCT ATAGGCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500
 TTAATACATA ACCTTATGTA TCATACACAT ACGATTTAGG TGACACTATA 550
 GAATAACATC CACTTTGCCT TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC 600
 AACTGCACCT CGGTTCTAAG CTTGGGCTGC AGGTCGCCGT GAATTTAAGG 650
 GACGCTGTGA AGCA 664

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 640 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150
CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200
GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250
CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300
CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
GGCTTTTTTTG GAGGCCTAGG CTTTGTGAAA AAGCTTATCC GGCCGGGAAC 400
GGTGCATTGG AACGCGGATT CCCC GTGCCA AGAGTCAGGT AAGTACCGCC 450
TATAGAGTCT ATAGGCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500
TTAATACATA ACCTTTTGA TCCTATAGAC TGACATCCAC TTTGCCTTTC 550
TCTCCACAGG TGTCCACTCC CAGGTCCAAC TGCACCTCGG TTCGAAGCTT 600
GGGCTGCAGG TCGCCGTGAA TTTAAGGGAC GCTGTGAAGC 640

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 646 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
 GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
 TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150
 CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200
 GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250
 CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300
 CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
 GGCTTTTTTTG GAGGCCTAGG CTTTTGCAAA AAGCTTATCC GGCCGGGAAC 400
 GGTGCATTGG AACGCGGATT CCCC GTGCCA AGAGTCAGGT AAGTACCGCC 450
 TATAGAGTCT ATAGGCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500
 TTAATACATA ACCTTTTGA TCCTACTAAC TACTGACTTA TTCTTTTCCT 550
 TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC AACTGCACCT CGGTTCGCGA 600
 AGCTTGGGCT GCAGGTCGCC GTGAATTTAA GGGACGCTGT GAAGCA 646

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 645 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
 GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
 TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150
 CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200
 GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250

(2) INFORMATION FOR SEQ ID NO:21:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

(2) INFORMATION FOR SEQ ID NO:22:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCAGGTAAGT ACTTGGATCC TATAGACTGA CATCCACTTT GCCTTTCTCT 50

CCACAGGT 58

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCAGGTAAGT ACTTGGATCC TACTAACTAC TGACTTATTC TTTTCCTTTC 50

TCTCCACAGG T 61

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCAGGTAAGT ACTTGGATCC TACTGACACT GACATCCACT TTTTCTTTTT 50

CTCCACAGGT 60